Amendments to the Claims:

This listing of claims will replace all prior versions, and listings, of claims in the application:

Listing of Claims:

1. (currently amended) A method of ~~detecting a polymorphic site in a sample to determine~~ determining alpha-2B-adrenergic receptor function~~,~~ by detecting a polymorphism at a polymorphic site in a polynucleotide encoding an alpha-2B-adrenergic receptor molecule, the method comprising:

   a. obtaining ~~the~~ a sample ~~having a~~ of a polynucleotide encoding an alpha-2B-adrenergic receptor molecule comprising SEQ ID NO: 1 or 2 or a fragment or a complement of the polynucleotide; and

   b. detecting in the sample a polymorphism at a polymorphic site comprising at least one of nucleotide positions 901 to 909 of SEQ ID NO: 1 or 2 ~~or fragment~~ or a complement thereof.

2. (currently amended) A method according to claim 1, wherein the ~~polymorphic site~~ polymorphism comprises SEQ ID NO: 3 or 4 or a complement thereof.

3. (currently amended) A method according to claim 2, wherein the ~~polymorphic site~~ polymorphism is an insertion of 9 nucleotides at nucleotide position 901 to 909 of SEQ ID NO: 1.

4. (currently amended) A method according to claim 2, wherein the ~~polymorphic site~~ polymorphism is a deletion of 9 nucleotides at nucleotide position 901 to 909 of SEQ ID NO: 2.

5. (currently amended) A method according to claim 2, wherein the complement of the ~~polymorphic site~~ polymorphism comprises SEQ ID NO: 5 or 6.

6. (currently amended) A method of genotyping an alpha-2B-adrenergic receptor gene comprising:

a. obtaining a sample having a polynucleotide encoding an alpha-2B-adrenergic receptor molecule comprising SEQ ID NO: 1 or 2 or a fragment or a complement of the polynucleotide; and

b. detecting in the sample a polymorphism at a polymorphic site comprising at least one of nucleotide positions 901 to 909 of SEQ ID NO: 1 or 2 ~~or fragment~~ or a complement thereof.

7. (currently amended) A method according to claim 6, wherein the genotyping is performed on two copies of the alpha-2B-adrenergic receptor gene.

8. (currently amended) A method according to claim 6, wherein the ~~polymorphic site~~ polymorphism comprises SEQ ID NO: 3 or 4 or a complement thereof.

9. (currently amended) A method according to claim 6, wherein the ~~polymorphic site~~ polymorphism is an insertion of 9 nucleotides at nucleotide positions 901 to 909 of SEQ ID NO: 1.

10. (currently amended) A method according to claim 6, wherein the ~~polymorphic site~~ polymorphism is a deletion of 9 nucleotides at nucleotide position 901 to 909 of SEQ ID NO: 2.

11. (currently amended) A method according to claim 6, wherein the complement of the ~~polymorphic site~~ polymorphism comprises SEQ ID NO: 5 or 6.

12. (currently amended) A method according to claim 6, wherein the detection of the ~~polymorphic site~~ polymorphism is by dideoxy sequencing, restriction digestion, allele-specific polymerase reaction, single-stranded conformational polymorphism analysis, genetic bit analysis, temperature gradient gel electrophoresis, ligase chain

reaction, ligase/polymerase genetic bit analysis, or random amplification of DNA.

13. (currently amended) A method of genotyping a polynucleotide encoding an alpha-2B-adrenergic receptor molecule from a sample, comprising: (a) obtaining a sample comprising the polynucleotide; and (b) performing a primer extension reaction employing an oligonucleotide comprising at least one nucleotide comprising a nucleotide sequence homologous to a nucleotide sequence located at position 901 to 909 of SEQ ID NO: 1 or 2 ~~or fragment~~ or a complement thereof.

14. (currently amended) A method according to claim 13, wherein the oligonucleotide comprises a nucleotide sequence having a length of from about 10 to about 50 nucleotides.

15. (original) A method according to claim 13, wherein the primer extension reaction is a single nucleotide primer extension reaction.

16. (currently amended) A method of genotyping an individual by genotyping a polynucleotide encoding an alpha-2B-adrenergic receptor molecule from a sample of ~~an~~ the individual, comprising:

a. isolating from the individual a ~~the~~ sample having a polynucleotide encoding an ~~the~~ alpha-2B adrenergic receptor molecule comprising SEQ ID NO: 1 or 2 or a fragment or a complement of the polynucleotide ~~thereof~~;

b. subjecting ~~incubating~~ the polynucleotide to an incubation with at least one oligonucleotide, the at least one oligonucleotide having a nucleotide sequence that is complementary to a region of the polynucleotide, and which, when hybridized to the region permits the identification of the nucleotide present at a polymorphic site of the polynucleotide, wherein the incubation is under conditions sufficient to allow specific hybridization to occur between complementary nucleic acid molecules;

c. permitting ~~the~~ hybridization to occur; and

d. identifying the polymorphic site to obtain the genotype of the individual, wherein the polymorphic site comprises a polymorphism comprising an insertion or deletion of 9 nucleotides at nucleotide positions 901 to 909 of SEQ ID NO: 1 or 2.

17. (currently amended) ~~A~~ The method according to claim 16, further comprising amplifying the ~~polymorphic site~~ polymorphism of the polynucleotide prior to the hybridization.

18. (currently amended) ~~A~~ The method according to claim 16, wherein the at least one oligonucleotide is selected from the group consisting of

5'-GCTCATCATCCCTTTCTCGCT-3' (SEQ ID NO: 13);

5'- AAAGCCCCACCATGGTCGGGT-3' (SEQ ID NO: 14);

5'-CTGATCGCCAAACGAGCAAC-3' (SEQ ID NO: 15*);*

5'-AAAAACGCCAATGACCACAG-3' (SEQ ID NO: 16);

5-'TGTAAAACGACGGCCAGT-3' (SEQ ID NO: 17);

5'-CAGGAAACAGCTATGACC-3' (SEQ ID NO: 18);

5'-AGAAGGAGGGTGTTTGTGGGG-3' (SEQ ID NO: 19);

5'- ACCTATAGCACCCACGCCCCT-3'(SEQ ID NO: 20);

5'-GGCCGACGCTCTTGTCTAGCC-3' (SEQ ID NO: 21);

5'-CAAGGGGTTCCTAAGATGAG-3' (SEQ ID NO: 22); and complementary sequences thereof.

19. (currently amended) ~~A~~ The method according to claim 16, wherein the specific

hybridization is selected from the group consisting of southern blot, dot blot, reverse dot blot, northern blot, and allele-specific oligonucleotide hybridization.

20. (currently amended) ~~A~~ The method according to claim 16, wherein the at least one oligonucleotide is labeled with a label selected from the group consisting of radiolabel, fluorescent label, bioluminescent label, chemilu.minescent label, nucleic acid label, hapten label, and enzyme label.

21. (currently amended) ~~A~~ The method according to claim 16, wherein the identity of the polymorphic site is determined by dideoxy sequencing, restriction digestion, allele-specific polymerase reaction, single-stranded conformational polymorphism analysis, genetic bit analysis, temperature gradient gel electrophoresis, ligase chain reaction, or ligase/polymerase genetic bit analysis, or random amplification of DNA.

22. (currently amended) ~~A~~ The method according to claim 16, wherein the at least one oligonucleotide ~~comprises a nucleotide sequence~~ is from about 10 to about 50 nucleotides in length.

23. (withdrawn) A method of detecting a polymorphic site in a sample to determine alpha-2B-adrenergic receptor function, comprising:

a. obtaining the sample having an alpha-2B-adrenergic receptor molecule comprising amino acid SEQ ID NO: 7 or 8 or fragment thereof and

b. detecting in the sample the polymorphic site at amino acid positions 294 to 309 of SEQ ID NO: 7 or 8.

24. (withdrawn) A method according to claim 23, wherein the polymorphic site comprises SEQ ID NO: 9 or 10.

25. (withdrawn) A method according to claim 23, wherein the polymorphic site is an insertion of 3 glutamic acids at amino acid positions 301 to 303 of SEQ ID NO: 7.

26. (withdrawn) A method according to claim 27, wherein the polymorphic site is a deletion of 3 glutamic acids at amino acid positions 301 to 303 of SEQ ID NO: 8.

27. (withdrawn) A method of detecting a polymorphic site to determine alpha-2B-adrenergic receptor function, comprising:

a. obtaining a sample having an alpha-2B-adrenergic receptor molecule comprising amino acid SEQ ID NO: 7 or 8 or fragment thereof;

b. contacting the sample with an antibody specifically reactive with the polymorphic site at amino acid positions 294 to 309 of SEQ ID NO: 7 or 8; and

c. detecting in the sample a complex formed between the antibody and amino acid positions 294 to 309 of SEQ ID NO: 7 or 8.

28. (withdrawn) A method according to claim 27, wherein the polymorphic site is an insertion of 3 glutamic acids at amino acid positions 301 to 303 of SEQ ID NO: 7.

29. (withdrawn) A method according to claim 27, wherein the polymorphic site is a deletion of 3 glutamic acids at amino acid positions 301 to 303 of SEQ ID NO: 8.

30. (currently amended) A method of haplotyping an alpha-2B-adrenergic receptor gene, wherein the gene exists as a first copy and a second copy, the method comprising:

a. obtaining a sample having apolynuclotide encoding an alpha-2B-adrenergic receptor molecule comprising SEQ ID NO: 1 or 2 or a fragment or a complement of the polynucleotide;

b. detecting in the sample a polymorphism at a polymorphic site comprising nucleotide positions 901 to 909 of SEQ ID NO: 1 or 2 or a fragment or a complement thereof on ~~one~~ a first copy of the alpha-2B-adrenergic receptor gene; and

c. determining the identity of an additional polymorphic site on the first copy of the alpha-2B-adrenergic receptor gene.

31. (currently amended) A method for ~~determining~~ identifying an individual at increased risk for developing a disease associated with an alpha-2B-adrenergic receptor molecule comprising:

a. obtaining a sample having a polynucleotide encoding an alpha-2B-adrenergic receptor molecule comprising SEQ ID NO: 1 or 2 or a fragment or a complement of the polynucleotide from the individual; and

b. detecting in the sample a polymorphism at a polymorphic site comprising at least one of nucleotide positions 901 to 909 of SEQ ID NO: 1 or 2 ~~or fragment~~ or a complement thereof, ~~which~~ wherein the polymorphism correlates to the disease, thereby identifying the individual at increased risk for the disease.

32. (currently amended) ~~A~~ The method of claim 31, wherein the disease is selected from the group consisting of cardiovascular disease, central nervous system disease, and combinations thereof.

33. (currently amended) ~~A~~ The method according to claim 31, wherein the ~~polymorphic site~~ polymorphism comprises SEQ ID NO: 3 or 4 or a complement thereof.

34. (currently amended) ~~A~~ The method according to claim 31, wherein the ~~polymorphic site~~ polymorphism is an insertion of 9 nucleotides at nucleotide position 901 to 909 of SEQ ID NO: 1.

35. (currently amended) ~~A~~ The method according to claim 31, wherein the ~~polymorphic site~~ polymorphism is a deletion of 9 nucleotides at nucleotide position 901 to 909 of SEQ ID NO: 2.

36. (currently amended) ~~A~~ The method according to claim 33, wherein the complement

of the ~~polymorphic site~~ polymorphism comprises SEQ ID NO: 5 or 6.

37. (currently amended) ~~A~~ The method according to claim 31, wherein the alpha-2B-adrenergic receptor molecule comprises SEQ ID NO. 7 or 8 or a fragment thereof.

38. (currently amended) A method for diagnosing or prognosing an individual with a disease associated with an alpha-2B-adrenergic receptor molecule, comprising:

a. obtaining a sample having a polynucleotide encoding an alpha-2B-adrenergic receptor molecule comprising SEQ ID NO: 1 or 2 or a fragment or a complement of the polynucleotide from the individual; and

b. detecting in the sample a polymorphism at a polymorphic site comprising at least one of nucleotide positions 901 to 909 of SEQ ID NO: 1 or 2 ~~or fragment~~ or a complement thereof which correlates to the disease~~, thereby diagnosing or prognosing the disease~~.

39. (currently amended) ~~A~~ The method according to claim 38, wherein the disease is a cardiovascular disease, a central nervous system disease, or combinations thereof.

40. (currently amended) ~~A~~ The method according to claim 38, wherein the ~~polymorphic site~~ polymorphism comprises SEQ ID NO: 3 or 4 or a complement thereof.

41. (currently amended) ~~A~~ The method according to claim 38, wherein the ~~polymorphic site~~ polymorphism is an insertion of 9 nucleotides at nucleotide position 901 to 909 of SEQ ID NO: 1.

42. (currently amended) ~~A~~ The method according to claim 38, wherein the ~~polymorphic site~~ polymorphism is a deletion of 9 nucleotides at nucleotide position 901 to 909 of SEQ ID NO: 2.

43. (currently amended) ~~A~~ The method according to claim 40, wherein the complement of the ~~polymorphic site~~ polymorphism comprises SEQ ID NO: 5 or 6.

44. (currently amended) ~~A~~ The method according to claim 38, wherein the alpha-2B adrenergic receptor molecule comprises SEQ ID NO: 7 or 8 or a fragment thereof.

45. (withdrawn) A method of predicting an individual's response to an agonist or antagonist, comprising:

a. obtaining a sample having a polynucleotide encoding an alpha-2B-adrenergic receptor molecule comprising SEQ ID NO: 1 or 2 or fragment or complement of the polynucleotide from the individual;

b. detecting in the sample a polymorphic site comprising nucleotide positions 901 to 909 of SEQ ID NO: 1 or 2 or fragment or complement thereof; and

c. correlating the polymorphic site to a predetermined response thereby predicting the individual's response to the agonist or antagonist.

46. (withdrawn) A method according to claim 45, wherein the alpha-2B adrenergic receptor molecule comprises SEQ ID NOS. 7 or 8 or fragment thereof.

47. (withdrawn) A method according to claim 45, wherein the agonist is an alpha-2B adrenergic receptor agonist.

48. (withdrawn) A method according to claim 45, wherein the antagonist is an alpha-2B adrenergic receptor antagonist.

49. (withdrawn) A method according to claim 47, wherein the alpha-2B adrenergic receptor agonist is an agonist selected from the group consisting of epinephrine, norepinephrine, clonidine, oxymetazoline, guanabenz, UK14304, BHT933 and combinations thereof.

50. (withdrawn) A method according to claim 48, wherein the alpha-2B adrenergic receptor antagonist is an antagonist selected from the group consisting of yohimbine,

prazosin, ARC 239, rauwolscine, idazoxan, tolazoline, phentolamine and combinations thereof.

51. (withdrawn) A method according to claim 45, wherein the predetermined response to the agonist or antagonist is correlated to adenyly cyclase, MAP kinase activity, phosphorylation or inositol phosphate levels.

52. (withdrawn) A method according to claim 45, wherein the individual is homozygous for SEQ ID NO: 2 and exhibits a decreased response to the alpha-2B adrenergic receptor agonist.

53. (withdrawn) A method according to claim 45, wherein the individual's response is desensitization to the agonist or antagonist.

54. (withdrawn) A method according to claim 47, wherein the individual's response is desensitization to the alpha-2B-adrenergic receptor agonist.

55. (withdrawn) A method for selecting an appropriate pharmaceutical composition to administer to an individual having a disease associated with an alpha-2B adrenergic receptor molecule, comprising:

a. obtaining a sample having a polynucleotide encoding an alpha-2B-adrenergic receptor molecule comprising SEQ ID NO: 1 or 2 or fragment or complement of the polynucleotide from the individual;

b. detecting in the sample a polymorphic site comprising nucleotide positions 901 to 909 of SEQ ID NO: 1 or 2 or fragment or complement thereof; and

c. selecting the appropriate pharmaceutical composition based on the polymorphic site present.

56. (withdrawn) A method of claim 55, wherein the disease is a cardiovascular disease, a central nervous system disease or combinations thereof.

57. (withdrawn) A method according to claim 55, wherein the alpha-2B-adrenergic receptor molecule comprises SEQ ID NO. 7 or 8 or fragment thereof.

58. (withdrawn) A method according to claim 55, wherein the pharmaceutical composition is an alpha-2B-adrenergic receptor agonist or antagonist.

59. (withdrawn) A method according to claim 58, wherein the alpha-2B-adrenergic receptor agonist is an agonist selected from the group consisting of epinephrine, norepinephrine, clonidine, oxymetazoline, guanabenz, UK14304, BHT933, and combinations thereof.

60. (withdrawn) A method according to claim 58, wherein the alpha-2B adrenergic receptor antagonist is an antagonist selected from the group consisting of yohimbine, prazosin, ARC 239, rauwolscine, idazoxan, tolazoline, phentolamine and combinations thereof.

61. (withdrawn) A method according to claim 58, wherein the appropriate pharmaceutical composition to administer is correlated to adenyly cyclase, MAP kinase, phosphorylation or inositol phosphate activity.

62. (withdrawn) A method according to claim 55, wherein the individual is homozygous for SEQ ID NO: 2 and exhibits a decreased response to the alpha-2B adrenergic receptor agonist.

63. (currently amended) A method of ~~detecting a polymorphic site in a sample to determine~~ determining alpha-2B-adrenergic receptor function~~,~~ by indirectly detecting a polymorphism at a polymorphic site in a polynucleotide encoding an alpha-2B-adrenergic receptor molecule, the method comprising:

a. obtaining ~~the~~ a sample ~~having~~ comprising a polynucleotide encoding an alpha-2B-adrenergic receptor molecule, wherein the polynucleotide, or a fragment or a complement thereof, comprises ~~comprising~~ SEQ ID NO: 1 or 2 ~~or fragment or~~

~~complement of the polynucleotide~~; and

b. indirectly detecting in the sample the polymorphism at the polymorphic site comprising at least one of nucleotide positions 901 to 909 of SEQ ID NO: 1 or 2 ~~or fragment~~ or a complement thereof.

64. (withdrawn) A method of detecting a polymorphic site in a sample to determine alpha-2B-adrenergic receptor function, comprising:

a. obtaining the sample having an alpha-2B-adrenergic receptor molecule comprising amino acid SEQ ID NO: 7 or 8 or fragment thereof; and

b. indirectly detecting in the sample the polymorphic site at amino acid positions 294 to 309 of SEQ ID NO: 7 or 8.